

1	ACA	OTC	AGC	C	M	A	P	L	C	P	E	P	W	P	L	12
13	L	I	P	P	T	O	G	C	T	C	C	C	T	O	C	48
49	TTG	ATC	CCG	GCC	CCT	A	P	G	L	T	V	Q	L	L	S	28
29	L	L	L	L	M	P	V	H	P	Q	R	L	P	R	M	96
97	CTG	CTG	CTT	CTG	ATG	CCT	GTG	CAT	CCC	CAG	AGG	TTG	CCC	CGG	ATG	44
145	E	D	S	P	L	G	G	G	S	S	G	E	D	D	P	144
161	GAG	GAT	TCC	CCC	TTG	GGA	GGA	GCC	TCT	TCT	GGG	GAA	GAT	GAC	CCA	60
193	G	E	K	D	L	P	S	E	K	D	S	P	R	E	K	192
241	GGC	GAG	GAG	GAT	CTG	CCC	AGT	GAA	GAG	GAT	TCA	CCC	AGA	GAG	GAG	76
289	F	P	G	E	G	D	L	P	G	E	G	D	L	P	G	240
336	CCA	CCC	GGA	GAG	GAG	GAT	CTA	PCT	GGA	GAG	GAG	GAT	CTA	CCT	GGA	92
385	E	D	L	P	E	V	K	P	K	S	E	E	E	G	S	288
432	GAG	GAT	CTA	CCT	GAA	GTT	AAG	CCT	AAA	TCA	GAA	GAA	GAG	GCC	TCC	108
481	K	L	E	D	L	P	T	V	E	A	P	G	D	P	Q	336
529	AAG	TTA	GAG	GAT	CTA	CCT	ACT	GTT	GAG	GCT	GCT	GAA	GAA	GCT	GAA	124
577	P	Q	N	N	A	H	R	D	K	E	G	D	D	O	S	384
625	CCC	CAG	AAT	AAT	ACC	CAC	AGG	GAC	AAA	GAA	GGG	GAT	GAC	CAG	AGT	140
672	W	R	Y	O	G	D	P	P	W	P	R	V	S	P	A	432
720	TOG	CGC	TAT	GGA	GCC	GAC	CCG	CCC	TOG	CCC	CGG	GTG	TCC	CCA	TCC	156
768	A	G	R	P	Q	S	P	V	D	I	R	P	Q	L	A	480
816	GGC	GGC	GGC	TTG	CAG	TCC	CCG	GTG	GAT	ATC	CGC	CCC	CAG	CTC	GGC	172
864	TTC	TGC	CCG	GCC	CTG	CGC	CCC	CTG	GAA	CTC	CTG	GGC	TTC	CAG	CTC	528
912	P	L	P	E	L	R	L	R	N	N	G	H	S	V	Q	188
960	CCG	CTC	CCA	GAA	CTG	CGC	CTG	CGC	AAC	AAT	GGC	CAC	AGT	GTG	CAA	576
1008	T	L	P	F	G	L	E	M	A	L	G	P	G	R	E	204
1056	ACC	CTG	CCT	CCT	GGG	CTA	GAG	ATG	OCT	CTG	GGT	CCC	GGG	CGG	GAG	624
1104	R	A	L	Q	L	H	L	H	W	G	A	A	G	R	P	220
1152	CGG	GCT	CTG	CAG	CTG	CAT	CTG	CAC	TGG	GGG	GCT	GCA	GGT	CGT	CCG	672
1200	S	K	H	T	V	E	G	H	R	F	P	A	E	I	H	236
1248	TCG	GAG	CAC	ACT	GTG	GAA	GCC	CAC	CGT	TTC	CCT	GGC	GAG	ATC	CAC	720
1296	V	H	L	E	T	A	F	A	R	V	D	E	A	L	G	252
1344	GTT	CAC	CTC	AGC	ACC	GCC	TTT	GCC	AGA	GTT	GAC	GAG	GCC	TTG	GGG	768
1392	P	G	G	L	A	V	L	A	A	F	L	E	E	G	P	268
1440	CCG	GGA	GCC	CTG	GCC	GTG	TTG	GCC	GCC	TTT	CTG	GAG	GAG	GGC	CCG	816
1488	E	N	S	A	Y	E	O	L	L	S	R	L	E	E	I	284
1536	GAA	AAC	AGT	GCC	TAT	GAG	CAG	TTG	CTG	TCT	CGC	TTG	GAA	GAA	ATC	864
1584	K	E	G	S	E	T	Q	V	P	G	L	D	I	S	A	300
1632	GAG	GAA	GCC	TCA	GAG	ACT	GAG	GTG	CCA	GGA	CTG	GAC	ATA	TCT	GCA	912
1680	L	P	S	D	F	S	R	Y	F	Q	Y	E	G	S	L	316
1728	CTG	CCC	TCT	GAC	TTG	AGC	CGC	TAC	TTC	CAA	TAT	GAG	GGG	TCT	CTG	960
1776	T	P	P	C	A	O	G	V	I	W	T	V	F	N	Q	332
1824	ACA	CCG	CCC	TGT	GCC	CAG	GGT	GTG	ATC	TGG	ACT	GTG	TTT	AAC	CAG	1008
1872	V	M	L	S	A	K	Q	L	H	T	L	S	D	T	L	348
1920	GTG	ATG	CTG	AGT	GCT	AAG	CAG	CTC	CAC	ACC	CTC	TCT	GAC	ACC	CTG	1056
1968	G	P	G	D	S	R	L	Q	L	N	F	R	A	T	Q	364
2016	GGA	CCY	GGT	GAC	TCT	CGG	CTA	CAG	CTG	AAC	TTC	CGA	GGG	ACG	CAG	1104
2064	L	N	G	R	V	I	E	A	S	F	P	A	G	V	D	380
2112	TTG	AAT	GGG	CGA	GTG	ATT	GAG	GCC	TCC	TTC	CCT	GCT	GGA	GTG	GAC	1152
2160	S	P	R	A	A	E	P	V	Q	L	N	S	C	L	A	396
2208	AGT	CCT	CGG	GCT	GCT	GAG	CCA	GTG	CAG	CTG	AAT	TCC	TGC	CTG	GCT	1200
2256	G	D	I	L	A	L	V	F	G	L	L	F	A	V	T	412
2304	GGT	GAC	ATC	CTA	GCC	CTG	GTT	TTT	GCC	CTC	CTT	TTT	GCT	GTG	ACC	1248
2352	V	A	F	L	V	Q	M	R	R	Q	H	R	R	G	T	428
2400	GTG	GCG	TTC	CTT	GTG	CAG	ATG	AGA	AGG	CAG	CAC	AGA	AGG	GGA	ACC	1296
2448	G	G	V	S	Y	R	P	A	E	V	A	E	T	G	A	444
2496	GGG	GGT	GTG	AGC	TAC	COC	CCA	GCA	GAG	GTG	ACC	GAG	ACT	GGA	GCC	1344
2544	AGG	CTG	GAT	CTT	GGA	GAA	TGT	GAG	AAG	CCA	GCC	AGA	GGC	ATC	TGA	460
2592	GGA	GCC	GGT	AAC	TGT	CCT	GTG	CTG	CTC	ATT	ATG	CCA	CTT	CCT	TTT	1392
2640	TOG	CAA	GAA	ATT	TTT	TAA	AAT	AAA	TAT	TTA	TAA	T				1440
2688																1488
2736																1522

FIG. 1

A	B
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1	181
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94K -

67K -

43K -

30K -

20.1K -

FIG. 2.

A B C D



FIG. 3.

TOEFO 672260

A B C D E F

1.5 kb —



FIG. 4.

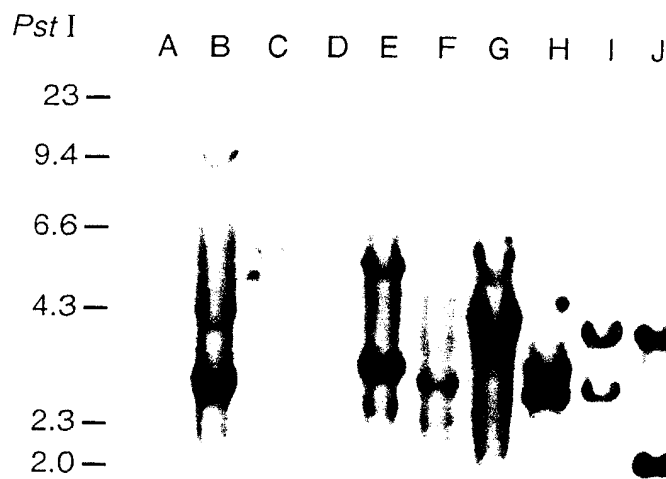


FIG._5

+

09772749 013004
T00E10 672260

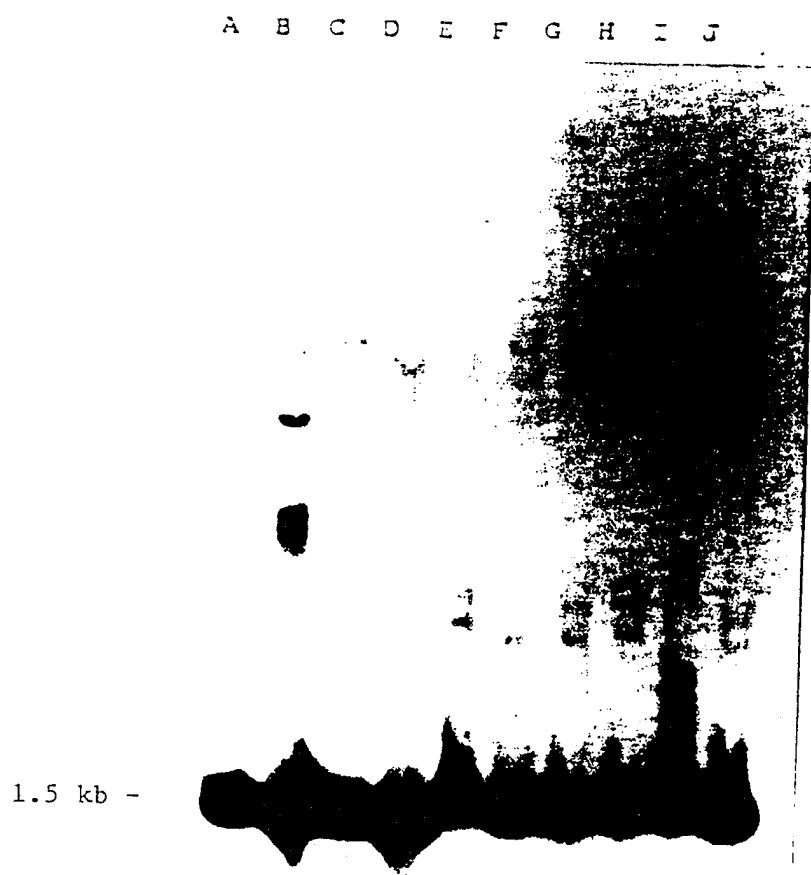


FIG. 5

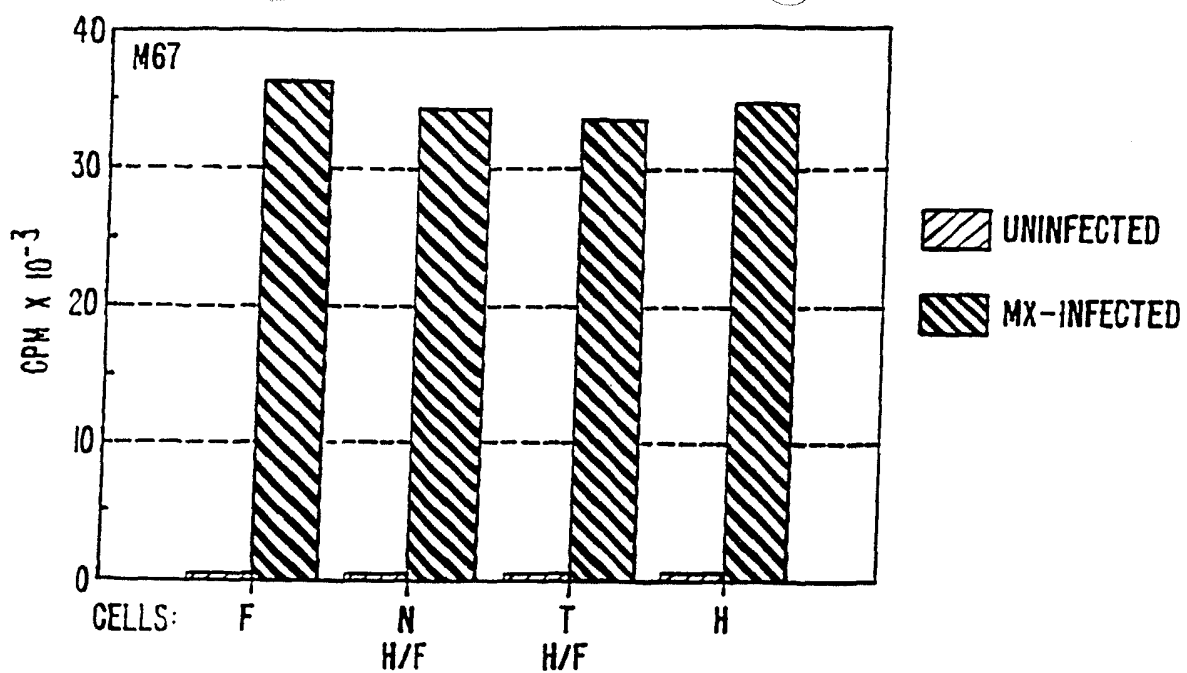


FIG. 6A.

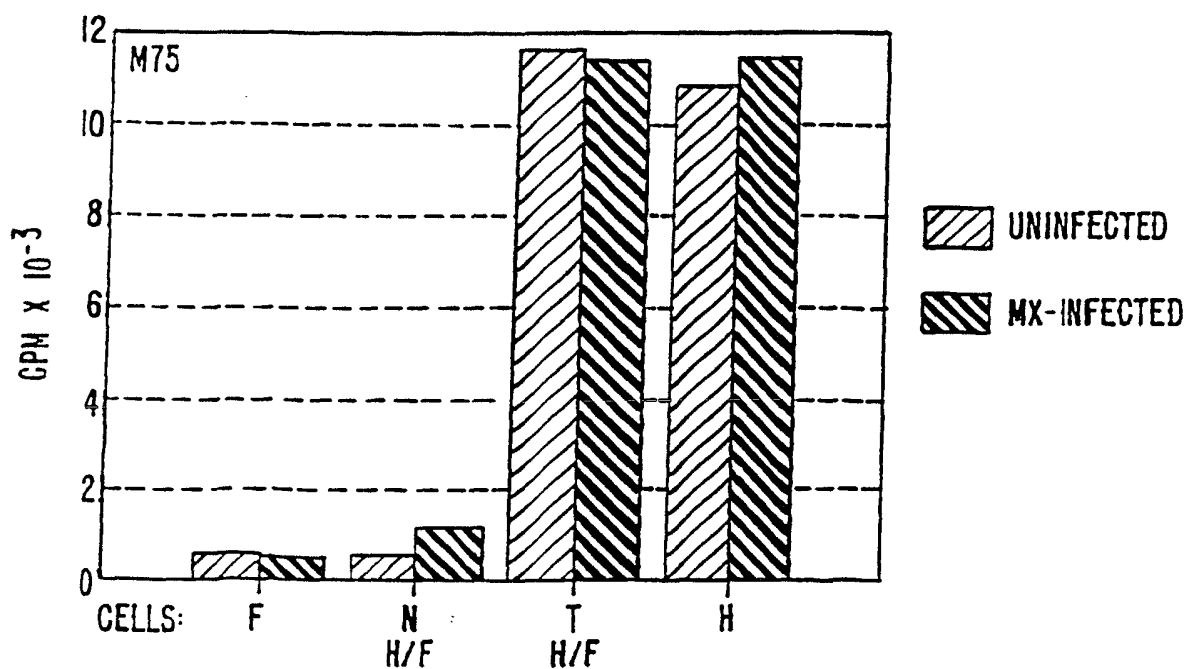


FIG. 6B.

FIG. 6A and 6B

007274 013004



1
2
3

HeLa K
+ MX

HeLa K

FIBR.

H/F-N

H/F-T

HeLa S

— 58k
— 54k

FIG. 7.

0072260

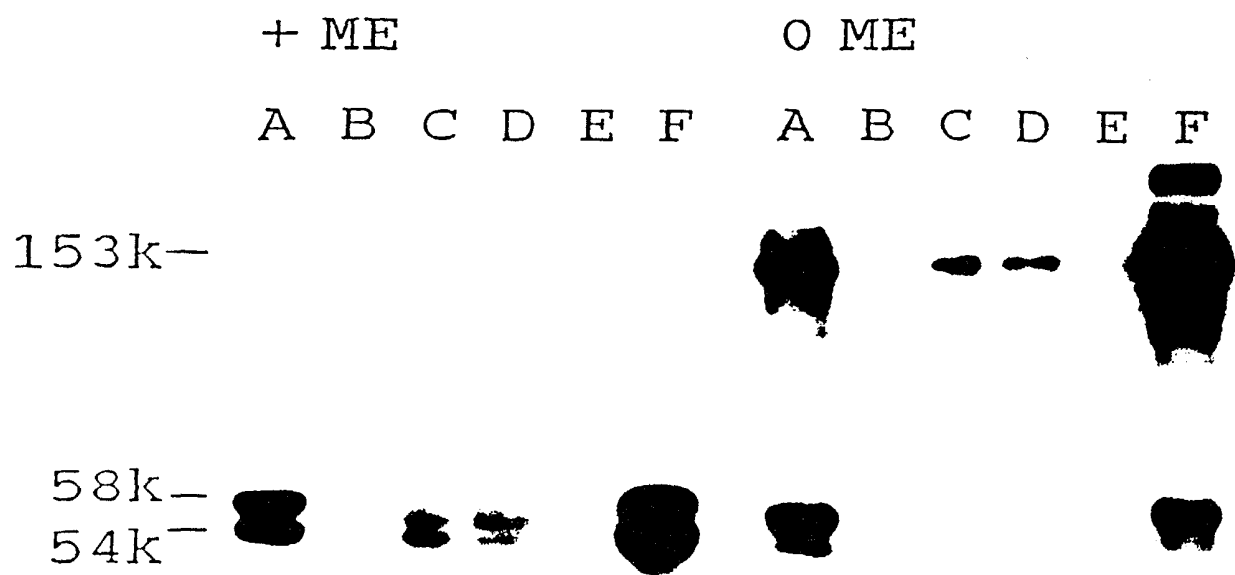


FIG. 8

TABLE 9

A B C D E F G H I J K L M N O P

58k-
54k-



-

FIG. 9.

OME

A	B
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FIG. 10.

[illegible]

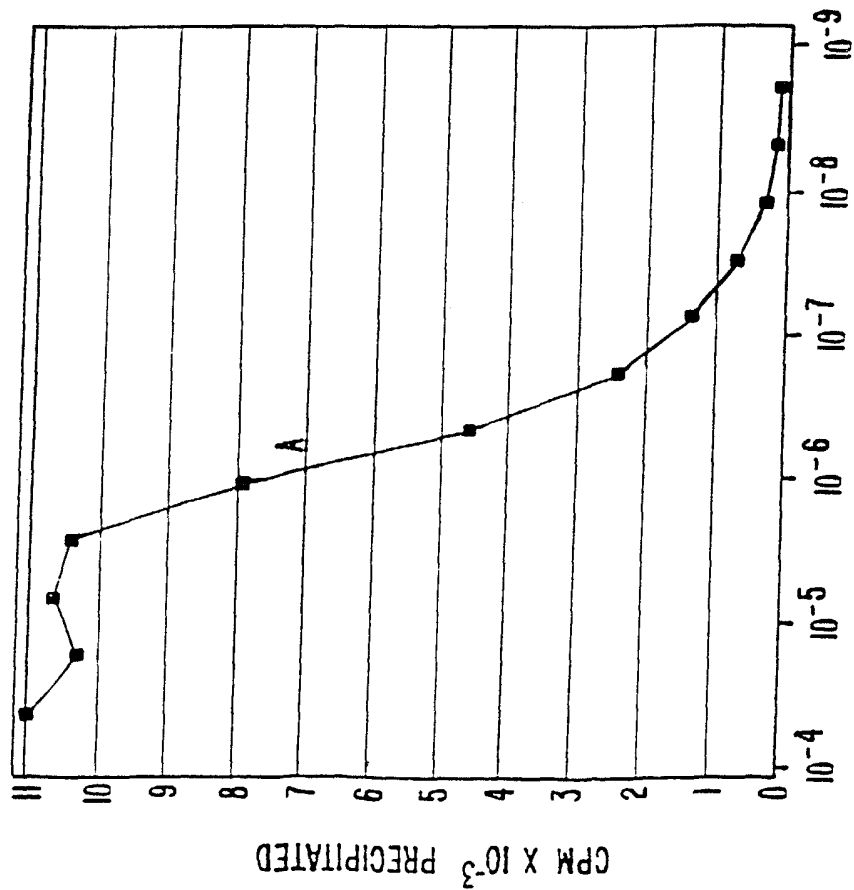


FIG. 11A.

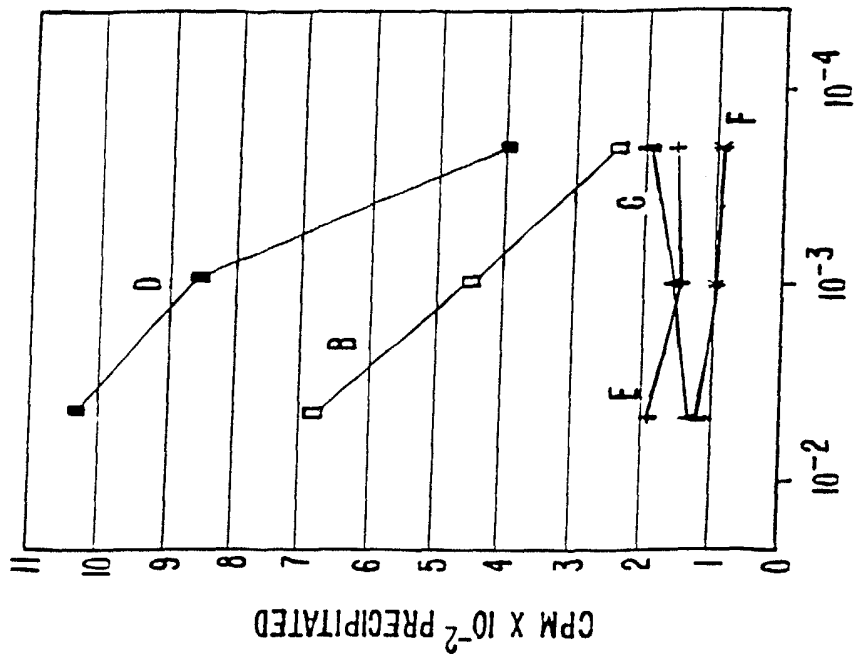


FIG. 11B.

TABLE 54460

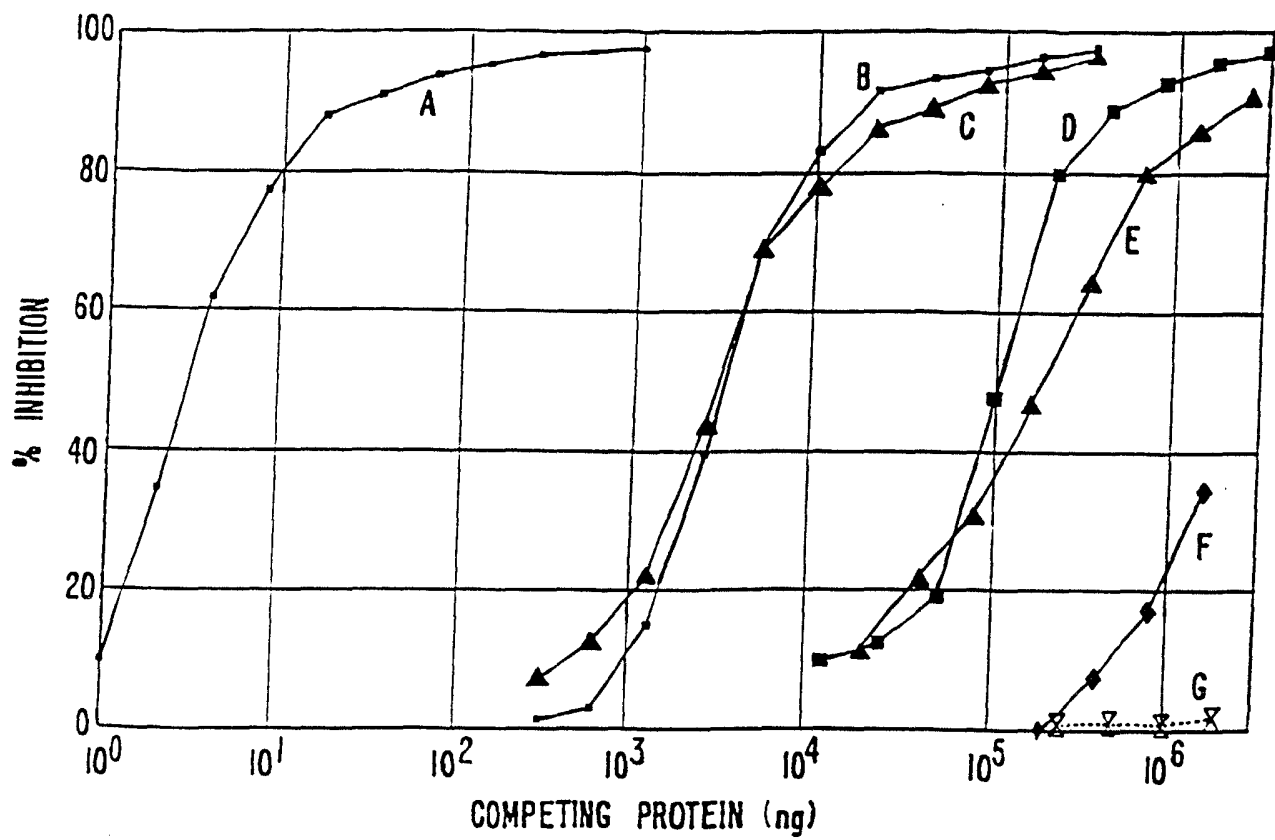


FIG. 12.



FIG. 13A.



FIG. 13B.



FIG. 13C.

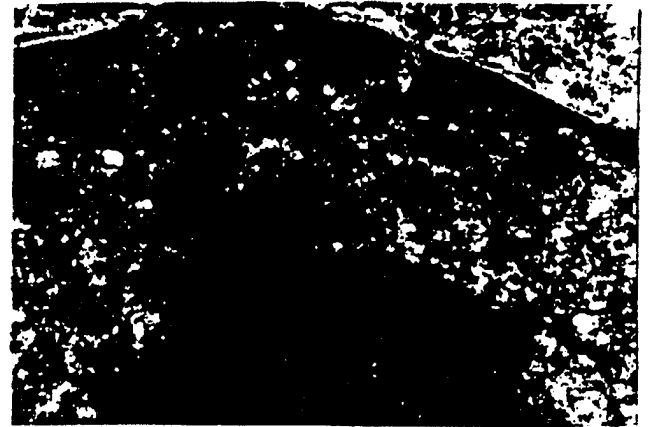


FIG. 13D.



FIG. 13E.

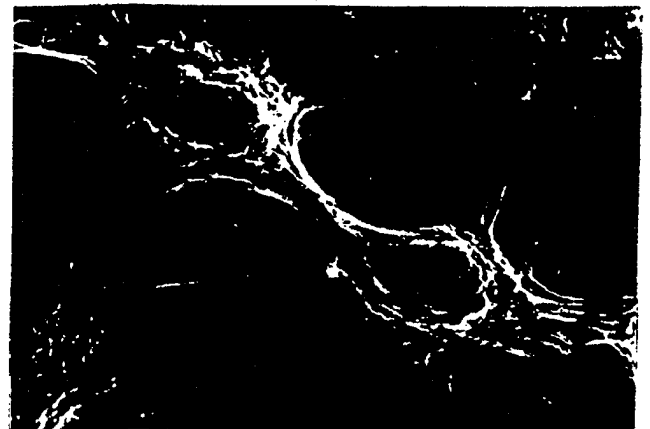


FIG. 13F.

097229-0400

REF ID: A62260

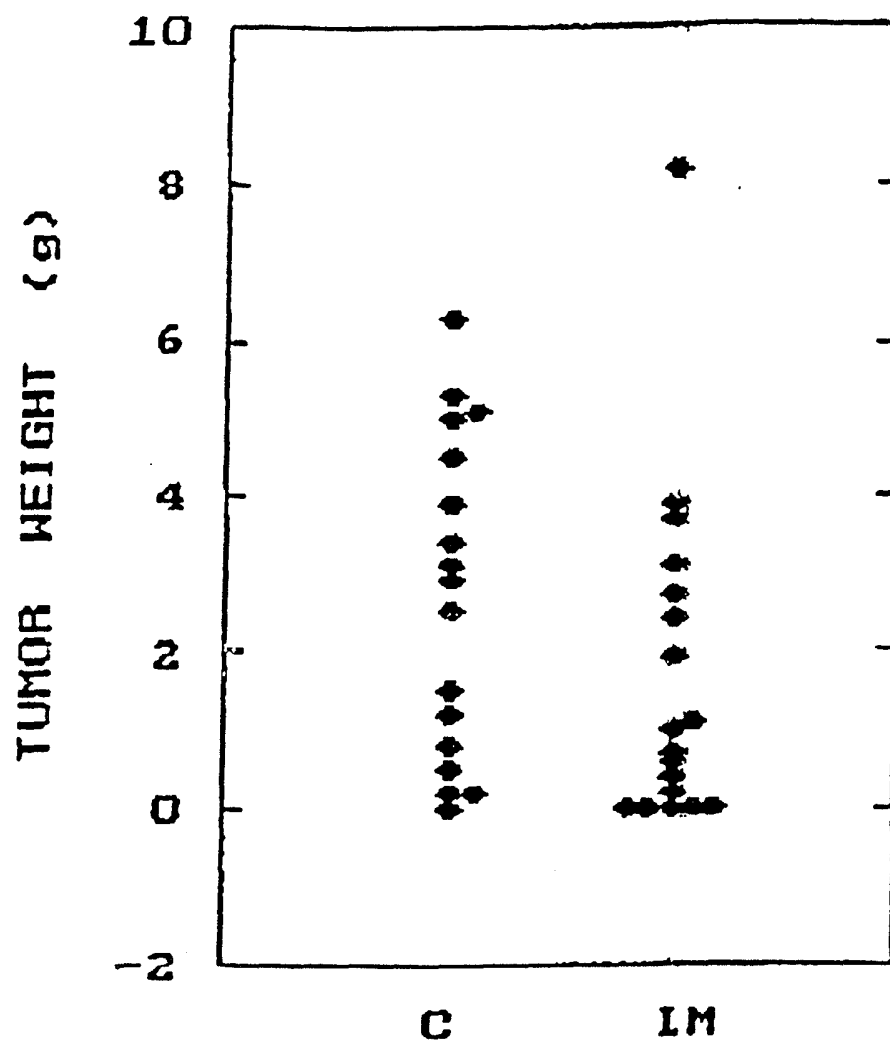


FIG. 14

3061	ggctccccta	gcaatgtgce	ctacctcttt	acctgctt	gggtggagtc	agggatgtat
3121	acatgagctg	ctttccctct	cagccagagg	acatgggggg	ccccagctcc	cctgcctttc
3181	cccttctgtg	cctggagctg	ggaagcaggg	caggggttagc	tgaggctggc	tggcaagcag
3241	ctgggtgggtg	ccagggagag	cctgcatagt	gccaggtgggt	gccttggggt	ccaagctagt
3301	ccatggcccc	gataaccttc	tgctgtgtgca	cacacctgcc	cctcactcca	ccccatcct
3361	agcttttggtg	tgggggagag	ggcacagggc	cagacaaacc	tgtgagactt	tggctccatc
3421	tctgcaaaaag	ggcgctctgt	gagtcagcct	gctccccctcc	aggcttgctc	ctccccacc
3481	cagctctcgt	ttccaatgca	cgtacagccc	gtacacacccg	tgtgctggga	caccccACAG
3541	TCAGCCGCAT	GGCTCCCCTG	TGCCCCAGCC	CCTGGCTCCC	TCTGTTGATC	CCGGCCCCCTG
3601	CTCCAGGCCT	CACTGTGCAA	CTGCTGCTGT	CACTGCTGCT	TCTGGTGCCT	GTCCATCCCC
3661	AGAGGTTGCC	CCGGATGCAG	GAGGATTCCC	CCTTGGGAGG	AGGCTCTTCT	GGGGAAGATG
3721	ACCCACTGGG	CGAGGAGGAT	CTGCCCAGTG	AAGAGGATTC	ACCCAGAGAG	GAGGATCCAC
3781	CCGGAGAGGA	GGATCTACCT	GGAGAGGAGG	ATCTACCTGG	AGAGGAGGAT	CTACCTGAAG
3841	TTAAGCCTAA	ATCAGAAGAA	GAGGGCTCCC	TGAAGTTAGA	GGATCTACCT	ACTGTTGAGG
3901	CTCCTGGAGA	TCCTCAAGAA	CCCCAGAATA	ATGCCCCACAG	GGACAAAGAA	Ggtaagtgggt
3961	catcaatctc	caaateccag	ttccaggagg	ttcatgactc	ccctcccata	ccccagccta
4021	ggctctgttc	actcagggaa	ggaggggaga	ctgtactccc	cacagaagcc	cttccagagg
4081	tcccatacca	atatccccat	ccccactctc	ggaggtagaa	agggacagat	gtggagagaa
4141	aataaaaagg	gtgcaaaaagg	agagaggtga	gctggatgag	atgggagaga	agggggagggc
4201	tggagaagag	aaagggatga	gaactgcaga	tgagagaaaa	aatgtgcaga	cagaggaaaa
4261	aaataggtgg	agaaggagag	tcagagagtt	tgaggggaag	agaaaaggaa	agcttgggag
4321	gtgaagtggg	taccagagac	aagcaagaag	agctggtaga	agtcactctca	tcttaggcta
4381	caatgaggaa	ttgagacctt	ggaagaaggg	acacagcagg	tagagaaacg	tggcttcttg
4441	actcccaagc	caggaattttg	gggaaagggg	ttggagacca	tacaaggcag	agggatgagt
4501	ggggagaaga	aagaaggag	aaaggaaaga	tgggtgactc	actcatttgg	gactcaggac
4561	tgaagtgcct	actcactttt	tttttttttt	tttttgagac	aaactttcac	ttttgttgcc
4621	caggctggag	tgcaatggcg	cgatctcggc	tcactgcaac	ctccacctcc	cgggttcaag
4681	tgattctcct	gcctcagcct	ctagccaagt	agctgcgatt	acaggcatgc	gccaccacgc
4741	ccggctaatt	tttgtatttt	tagtagagac	ggggtttcgc	catgttgggtc	aggctgggtct
4801	cgaactcctg	atctcaggtg	atccaaccac	cctggcctcc	caaagtgctg	ggattatagg
4861	cgtgagccac	agcgctggc	ctgaagcagc	cactcacttt	tacagacctt	aagacaatga
4921	ttgcaagctg	gtaggattgc	tgttttgccc	accagctgc	ggtgttgagt	ttgggtgcgg
4981	tctcctgtgc	tttgacactg	gcccgcctaa	ggcatttgtt	accgtaatg	ctcctgtaag
5041	gcactctcgt	ttgtgacatc	gttttgggtc	ccaggaaggg	attggggctc	taagcttgag
5101	cggttcatcc	ttttcattta	tacagGGGAT	GACCAGAGTC	ATTGGCGCTA	TGGAGgtgag
5161	acaccacacc	gctgcacaga	cccaatctgg	gaaccagct	ctgtggatct	ccccacagc
5221	cgteccctgaa	cactgggtccc	gggcgtccca	cccgccgccc	accgtcccac	ccctccacct
5281	tttctacccg	ggttccctaa	gttcctgacc	taggcgtcag	acttccctcac	tatactctcc
5341	caccccagGC	GACCCGCCCT	GGCCCCGGGT	GTCCCCAGCC	TGCGCGGGCC	GCTTCCAGTC
5401	CCCGGTGGAT	ATCCGCCCCC	AGCTCGCCGC	CTTCTGCCCCG	GCCCTGCGCC	CCCTGGAAC
5461	CCTGGGCTTC	CAGCTCCCCG	CGCTCCCAGA	ACTGCGCCTG	CGCAACAATG	GCCACAGTGg
5521	tgaggggggtc	tccccgccga	gacttggggg	tggggcgggg	cgcaggggaag	ggaaccgtcg
5581	cgcagtgctt	gcccgggggt	tgggctggcc	ctaccggggc	gggcccggctc	acttgcctct
5641	ccctacgcag	TGCAACTGAC	CCTGCCTCCT	GGGCTAGAGA	TGGCTCTGGG	TCCCGGGCGG
5701	GAGTACCGGG	CTCTGCAGCT	GCATCTGCAC	TGGGGGGCTG	CAGGTCTGTC	GGGCTCGGAG
5761	CACACTGTGG	AAGGCCACCG	TTTCCCTGCC	GAGgtgagcg	cggactggcc	gagaaggggc
5821	aaaggagcgg	ggcggacggg	ggccagagac	gtggccctct	cctaccctcg	tgtccttttc
5881	agATCCACGT	GGTTCACCTC	AGCACCgcct	TTGCCAGAGT	TGACGAGGCC	TTGGGGCGCC
5941	CGGGAGGCCT	GGCCGTGTTG	GCCGCCTTTC	TGGAGgtacc	agatcctgga	caccccctac
6001	tccccgcttt	cccatcccat	gctcctcccg	gactctatcg	tggagccaga	gaccccatcc
6061	cagcaagctc	actcaggccc	ctggetgaca	aactcattca	cgcactgttt	gttcatttaa
6121	cacccactgt	gaaccaggca	ccagccccc	acaaggattc	tgaagctgta	ggtccttgcc
6181	tctaaggagc	ccacagccag	tgggggaggg	tgacatgaca	gacacatagg	aaggacatag
6241	taaagatggt	ggtcacagag	gaggtgacac	ttaaagcctt	cactggtaga	aaagaaaagg

FIG. 15b

6301 aggtgttcat tgcagaggaa acagaatgtg caaagactca gaatatggcc tatttaggga
6361 atggctacat acaccatgat tagaggaggc ccagtaaagg gaagggatgg tgagatgcct
6421 gctaggttca ctcactcact tttattttat ttttattttt tttgacagtc tctctgtcgc
6481 ccaggctgga gtgcagtggg gtgatcttgg gtcactgcaa cttccgcctc ccgggttcaa
6541 gggattctcc tgcctcagct tcctgagtag ctgggggttac aggtgtgtgc caccatgccc
6601 agctaatttt tttttgtatt ttttagtagac aggggtttcac catgttgggtc aggtgtgtct
6661 caaactcctg gcctcaagtg atccgcctga ctcagcctac caaagtgtgtg attacaagtg
6721 tgagccaccg tgcccagcca cactcactga ttctttaatg ccagccacac agcacaaaagt
6781 tcagagaaat gcctccatca tagcatgtca atatgttcat actcttaggt tcatgatgtt
6841 cttaacatta ggttcataag caaaataaga aaaaagaata ataaataaaa gaagtggcat
6901 gtcaggacct cacctgaaaa gccaaacaca gaatcatgaa ggtgaatgca gaggtgacac
6961 caacacaaag gtgtatatat ggtttcctgt ggggagtagt tacggaggca gcagtgaagt
7021 agactgcaaa cgtcagaagg gcacgggtca ctgagagcct agtatcctag taaagtgggc
7081 tctctccctc tctctccagc ttgtcattga aaaccagtcc accaagcttg ttggttcgca
7141 cagcaagagt acatagagtt tgaaataata cataggattt taagagggag acactgtctc
7201 taaaaaaaaa aacaacagca acaacaaaaa gcaacaacca ttacaatttt atgttccctc
7261 agcattctca gagctgagga atgggagagg actatgggaa ccccttccat gttccggcct
7321 tcagccatgg ccctggatac atgcactcat ctgtcttaca atgtcattec cccagGAGGG
7381 CCCGGAAGAA AACAGTGCCT ATGAGCAGTT GCTGTCCTCG TTGGAAGAAA TCGCTGAGGA
7441 AGgtcagttt gttgggtctgg ccactaatct ctgtggccta gttcataaag aatcaccctt
7501 tggagcttca ggtctgaggg tggagatggg tgcctccag tgcaggaggg attgaagcat
7561 gagccagcgc tcatcttgat aataaccatg aagctgacag acacagttac ccgcaaacgg
7621 ctgcctacag attgaaaacc aagcaaaaac cgccgggcac ggtggctcac gcctgtaatc
7681 ccagcacttt gggaggccaa ggcaggtgga tcacgaggtc aagagatcaa gaccatcctg
7741 gccaacatgg tgaaacccca tctctactaa aaatacgaaa aaatagccag gcgtgggtggc
7801 ggggtgcctgt aatcccagct actcgggagg ctgaggcagg agaatggcat gaaccgggga
7861 ggcagaagtt gcagtgagcc gagatcgtgc cactgcactc cagcctgggc aacagagcga
7921 gactcttgtc tcaaaaaaaaa aaaaaaaaaa gaaaaccaag caaaaaccaa aatgagacaa
7981 aaaaaacaag accaaaaaat ggtgtttgga aattgtcaag gtcaagctcg gagagctaaa
8041 ctttttctga gaactgttta tctttaataa gcatcaaata ttttaacttt gtaaataactt
8101 ttgttggaat tctgttctct cttagtcaat ctggggtcat tttaaatctc acttactcta
8161 ctgacctttt taggtttctg cttagactagg tagaactctg ccttttgcatt tcttgtgtct
8221 gttttgtata gttatcaata ttcataattt tttacaagtt attcagatca ttttttcttt
8281 tctttttttt tttttttttt ttttttacat ctttagtaga gacagggttt caccatattg
8341 gccaggctgc tctcaaactc ctgaccttgt gatccaccag cctcggcctc ccaaagtgtc
8401 gggattcatt ttttcttttt aatttgctct gggcctaaac ttgtggccca gcactttatg
8461 atggtacaca gagttaagag tgtagactca gacggctctt cttcttctct tctcttctct
8521 cctcccttcc ctcccacctt ceettctctc cttcctttct ttcttctctc cttgttctct
8581 caggcctctt ccagttgtct caaagccctg taactttttt tgagttaacg tcttatggga
8641 agggcctgca cttagtgaag aagtgtctc agagttgagt taccttgggt tctgggaggt
8701 gaaactgtat ccctataccc tgaagcttta agggggtgca atgtagatga gacccaaca
8761 tagatcctct tcacagGCTC AGAGACTCAG GTCCCAGGAC TGGACATATC TGCACTCCTG
8821 CCTCTGACT TCAGCCGCTA CTCCAATAT GAGGGGTCTC TGACTACACC GCCCTGTGCC
8881 CAGGGTGTC TCTGGACTGT GTTTAACCAG ACAGTGATGC TGAGTGCTAA GCAGgtgggc
8941 ctgggggtgt tgtggacaca gtgggtgcgg gggaaagagg atgtaagatg agatgagaaa
9001 caggagaaga aagaaatcaa ggctgggctc tgtggcttac gcctataatc ccaccaggtt
9061 gggaggctga ggtgggagaa tggtttgagc ccaggagttc aagacaaggc ggggcaacat
9121 agtgtgaccc catctctacc aaaaaaaccc caacaaaacc aaaaatagcc gggcatgggt
9181 gtatgcggcc tagtcccagc tactcaagga ggctgaggtg ggaagatcgc ttgattccag
9241 gagtttgaga ctgcagtgag ctatgatccc accactgcct accatcttta ggatacattt
9301 atttatttat aaaagaaatc aagaggtctg atggggaata caggagctgg aggggtggagc
9361 cctgaggtgc tggttgtgag ctggcctggg acccttgttt cctgtcatgc catgaaccca
9421 cccacactgt ccactgacct ccctagCTCC ACACCTCTC TGACACCCTG TGGGGACCTG
9481 GTGACTCTCG GCTACAGCTG AACTTCCGAG CGACGCAGCC TTTGAATGGG CGAGTGATTG

FIG. 15c

9541	AGGCCTCCTT	CCCTGCTGGA	GTGGACAGCA	GTCCTCGGGC	TGCTGAGCCA	Ggtacagctt
9601	tgtctgggtt	ccccccagcc	agtagtccct	tatcctccca	tgtgtgtgcc	agtgtctgtc
9661	attgggtggtc	acagcccgcc	tctcacatct	cctttttctc	tccagTCCAG	CTGAATTCCT
9721	GCCTGGCTGC	TGgtgagtc	gccccctctc	ttggtcctga	tgccaggaga	ctcctcagca
9781	ccattcagcc	ccagggctgc	tcaggaccgc	ctctgetccc	tctccttttc	tgcagaacag
9841	accccaaccc	caatattaga	gaggcagatc	atgggtgggga	ttcccccat	gtccccagag
9901	gctaattgat	tagaatgaag	cttgagaaat	ctcccagcat	ccctctcgca	aaagaatccc
9961	cccccccttt	tttaaagata	gggtctcact	ctgtttgccc	caggctgggg	tgttgtggca
10021	cgatcatagc	tcactgcagc	ctcgaaactcc	taggctcagg	caatcctttc	accttagctt
10081	ctcaaagcac	tgggactgta	ggcatgagcc	actgtgcctg	gccccaaacg	gcccttttac
10141	ttggctttta	ggaagcaaaa	acggtgctta	tcttaccctc	tctcgtgtat	ccaccctcat
10201	cccttggtcg	gcctcttctg	gagactgagg	cactatgggg	ctgcctgaga	actcggggca
10261	ggggtgggtg	agtgcactga	ggcaggtggt	gaggaaactct	gcagaccctc	cttccttccc
10321	aaagcagccc	tctctgctct	ccatcgagc	TGACATCCTA	GCCCTGGTTT	TTGGCCTCCT
10381	TTTTGCTGTC	ACCAGCGTCG	CGTTCCTTGT	GCAGATGAGA	AGGCAGCACA	Ggtattacac
10441	tgaccctttc	ttcaggcaca	agcttcccc	acccttgtgg	agtcacttca	tgcaaagcgc
10501	atgcaaata	gctgctcctg	ggccagtttt	ctgattagcc	tttctgttg	tgtacacaca
10561	gAAGGGGAAC	CAAAGGGGGT	GTGAGCTACC	GCCCAGCAGA	GGTAGCCGAG	ACTGGAGCCT
10621	AGAGGCTGGA	TCTTGAGAGAA	TGTGAGAAGC	CAGCCAGAGG	CATCTGAGGG	GGAGCCGGTA
10681	ACTGTCCTGT	CCTGCTCATT	ATGCCACTTC	CTTTTAACTG	CCAAGAAATT	TTTTAAAATA
10741	AATATTTATA	ATaaaatatg	tgtagtcac	ctttgttccc	caaatacagaa	ggaggatatt
10801	gaatttccta	ttactgttat	tagcaccaat	ttagtggtaa	tgcattttatt	ctattacagt
10861	tcggcctcct	tccacacatc	actccaatgt	gttgctcc		

FIG. 15d

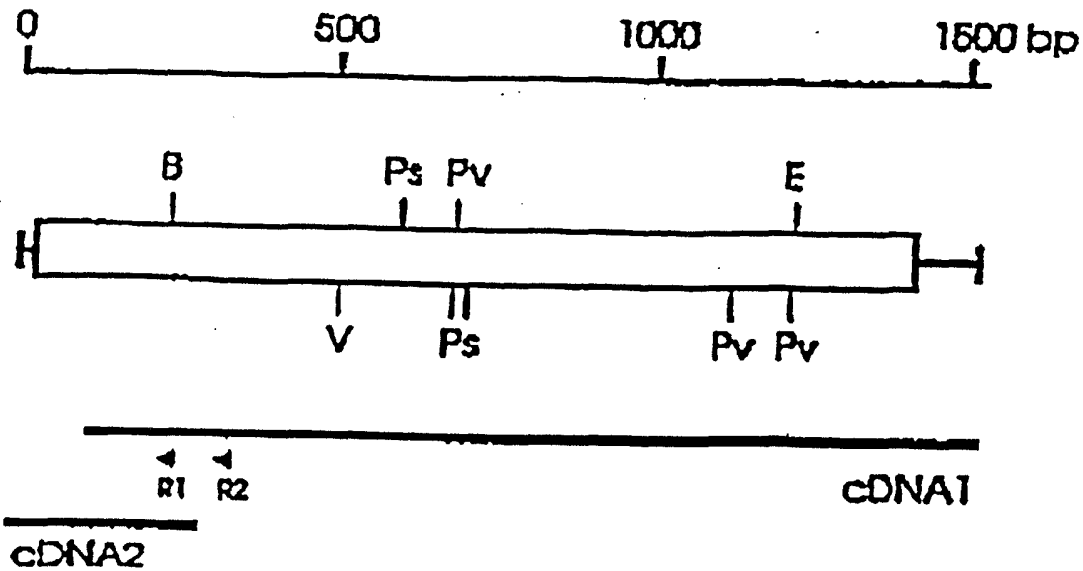


FIG. 16

09773710 09773710



FIG. 17

0072749-01001

1 2 3 4



<- 265 nt

FIG 18a

1 2 3 4



<- 124 nt

FIG. 18b

0072749-013004
T00E70-672260

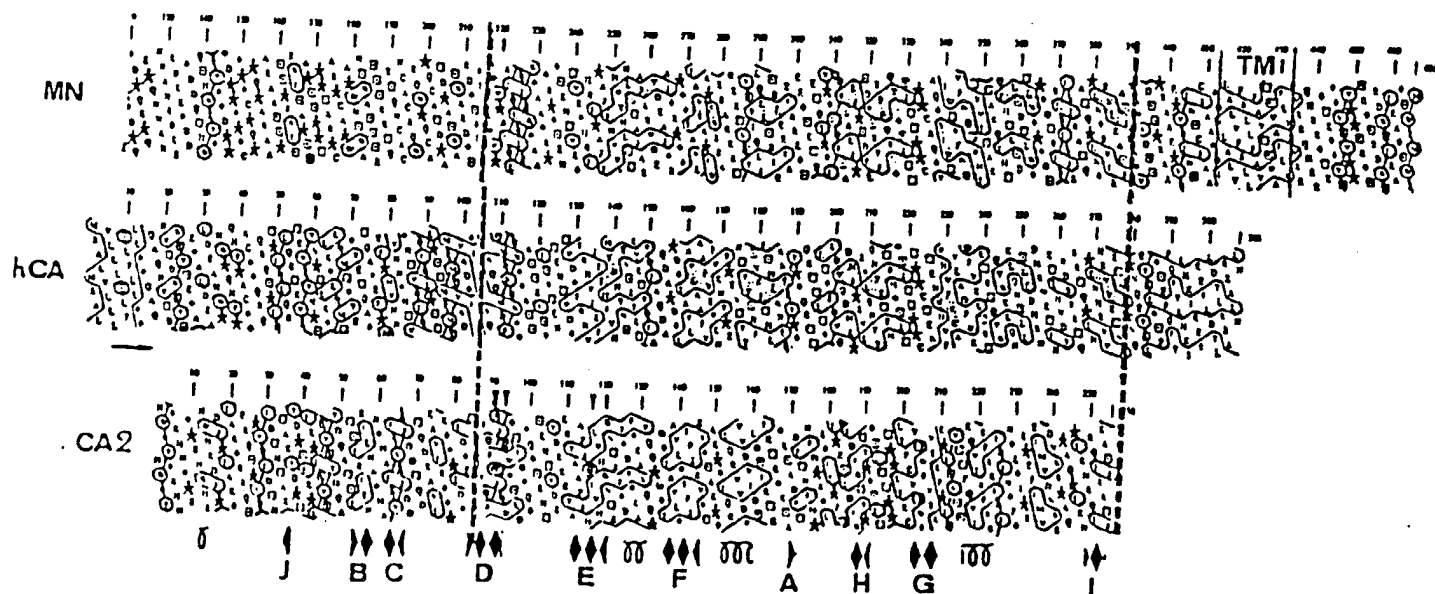


Fig. 19a

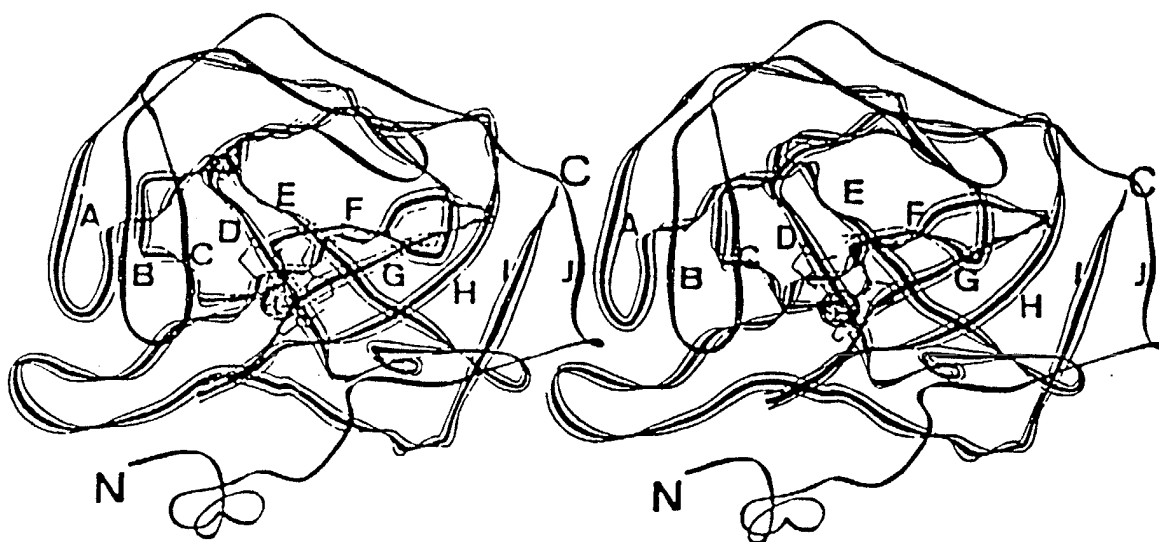


Fig. 19b

FIG. 20

5' MN Genomic Region

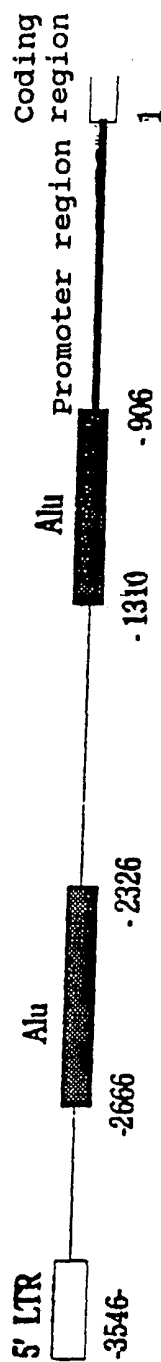


FIG. 20

0972749-013001

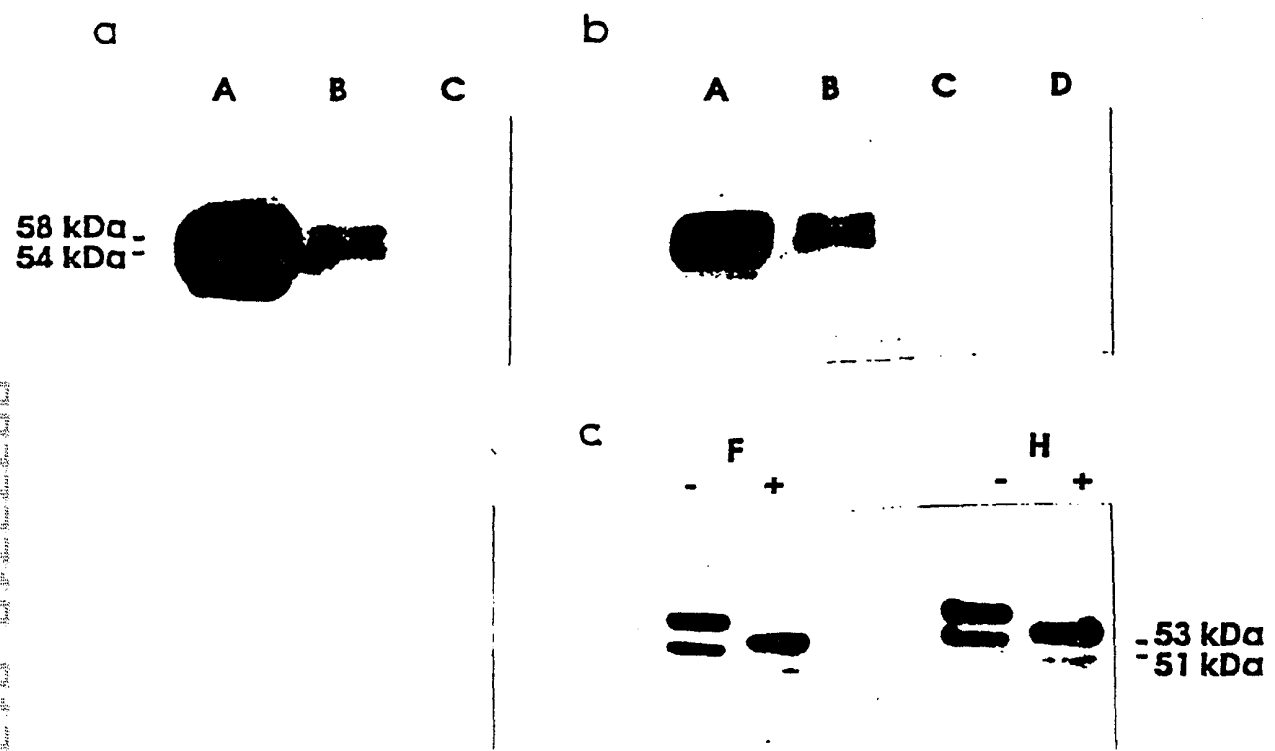


FIG. 21

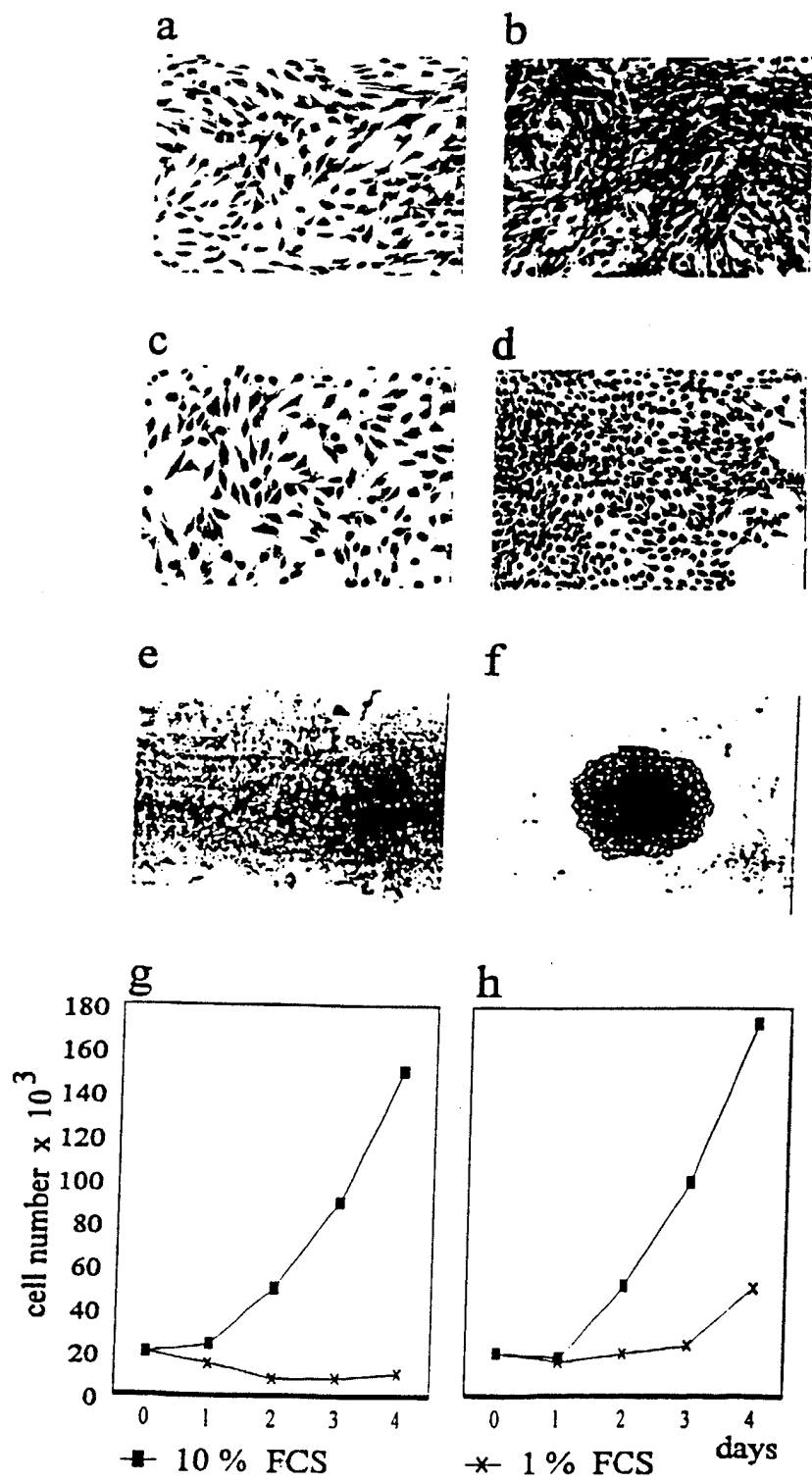


FIG. 22

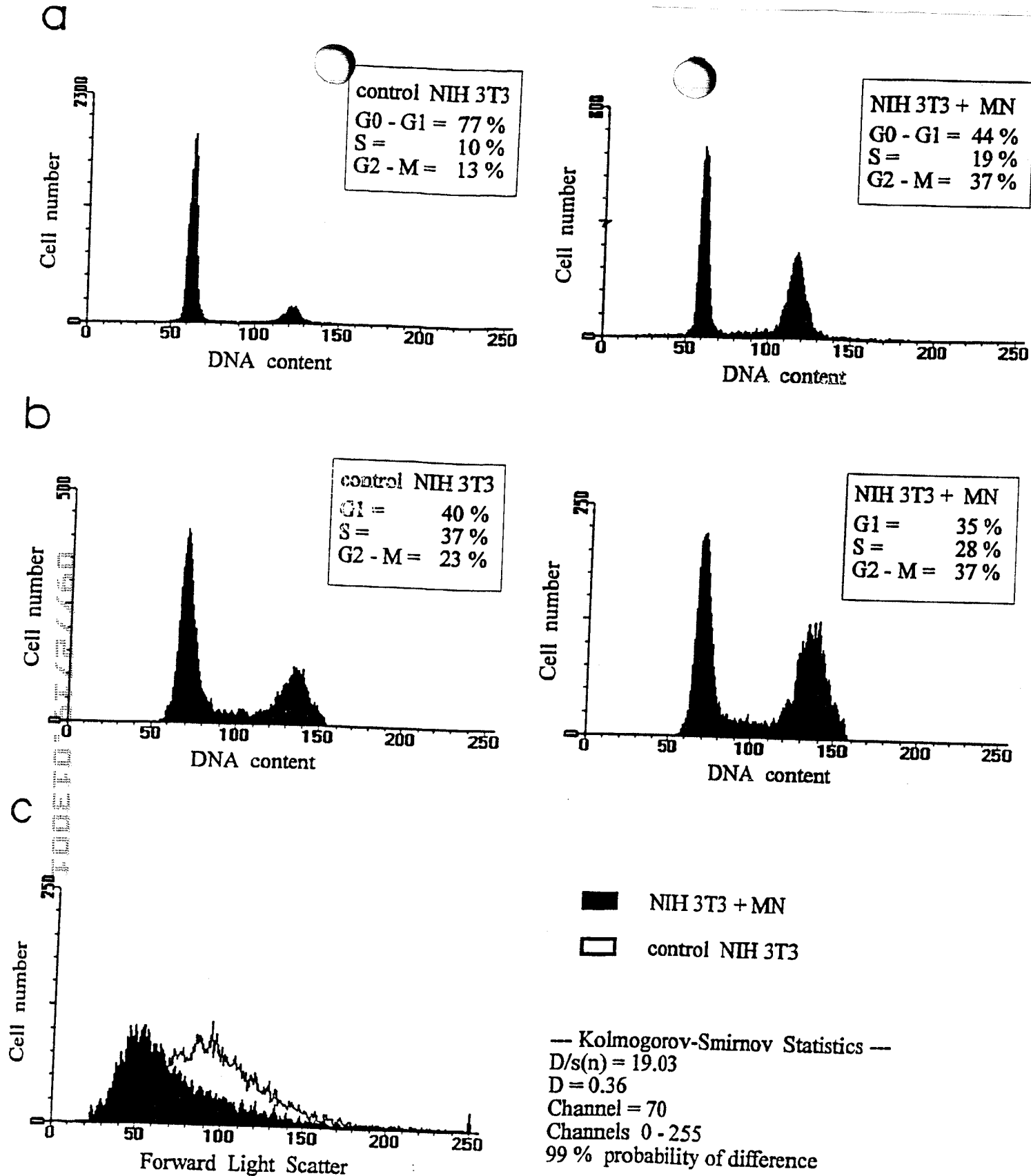


FIG. 23



FIG. 24

-506 CTTGCTTTTC ATTCAAGCTC AAGTTTGTCT CCCACATAACC CATTACTTAA CTCACCCCTCG

-446 GGCTCCCCTA GCAGCCTGCC CTACCTCTTT ACCTGCTTCC TGGTGGAGTC AGGGATGTAT
AP2 AP2

-386 ACATGAGCTG CTTTCCCTCT CAGCCAGAGG ACATGGGGGG CCCCAGCTCC CCTGCCTTTC

-326 CCCTTCTGTG CCTGGAGCTG GGAAGCAGGC CAGGGTTAGC TGAGGCTGGC TGGCAAGCAG

-266 CTGGGTGGTG CCAGGGAGAG CCTGCATAGT GCCAGGTGGT GCCTTGGGTT CCAAGCTAGT
p53

-206 CCATGGCCCC GATAACCTTC TGCCTGTGCA CACACCTGCC CCTCACTCCA CCCCATCCT
Inr

-146 AGCTTTGGTA TGGGGGAGAG GGCACAGGGC CAGACAAACC TGTGAGACTT TGGCTCCATC
Inr

-86 TCTGCAAAAG GGCCTCTGT GAGTCAGCCT GCTCCCCTCC AGGCTTGCTC CTCCCCCACC
AP1 p53 AP2

-26 CAGCTCTCGT TTCCAATGCA CGTACAGCCC GTACACACCG TGTGCTGGGA CACCCCACAG

FIG. 25

TOE TO 672/50

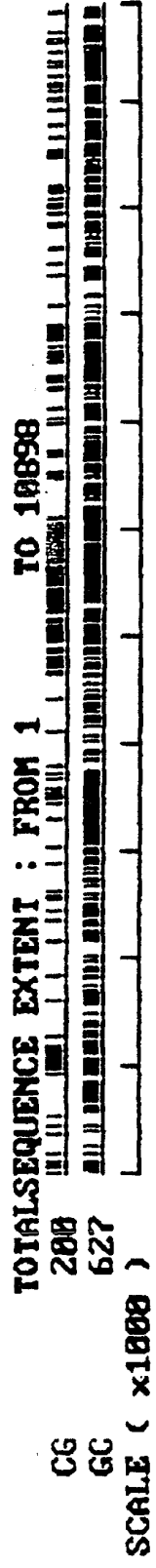


FIG. 26

TOBETD-5T2460

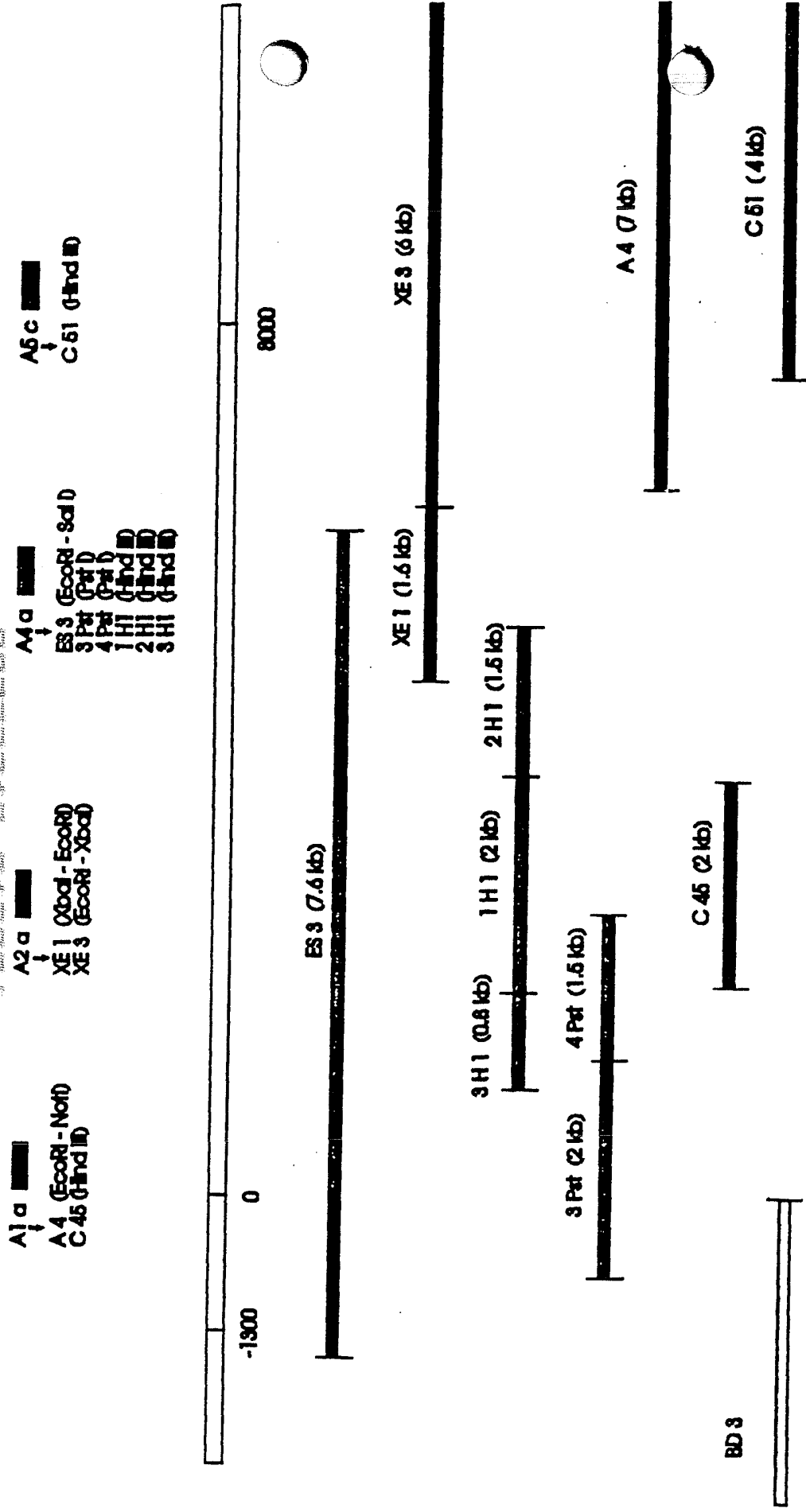


FIG. 27

CLONING OF MN-PROMOTER-CAT CONSTRUCTS

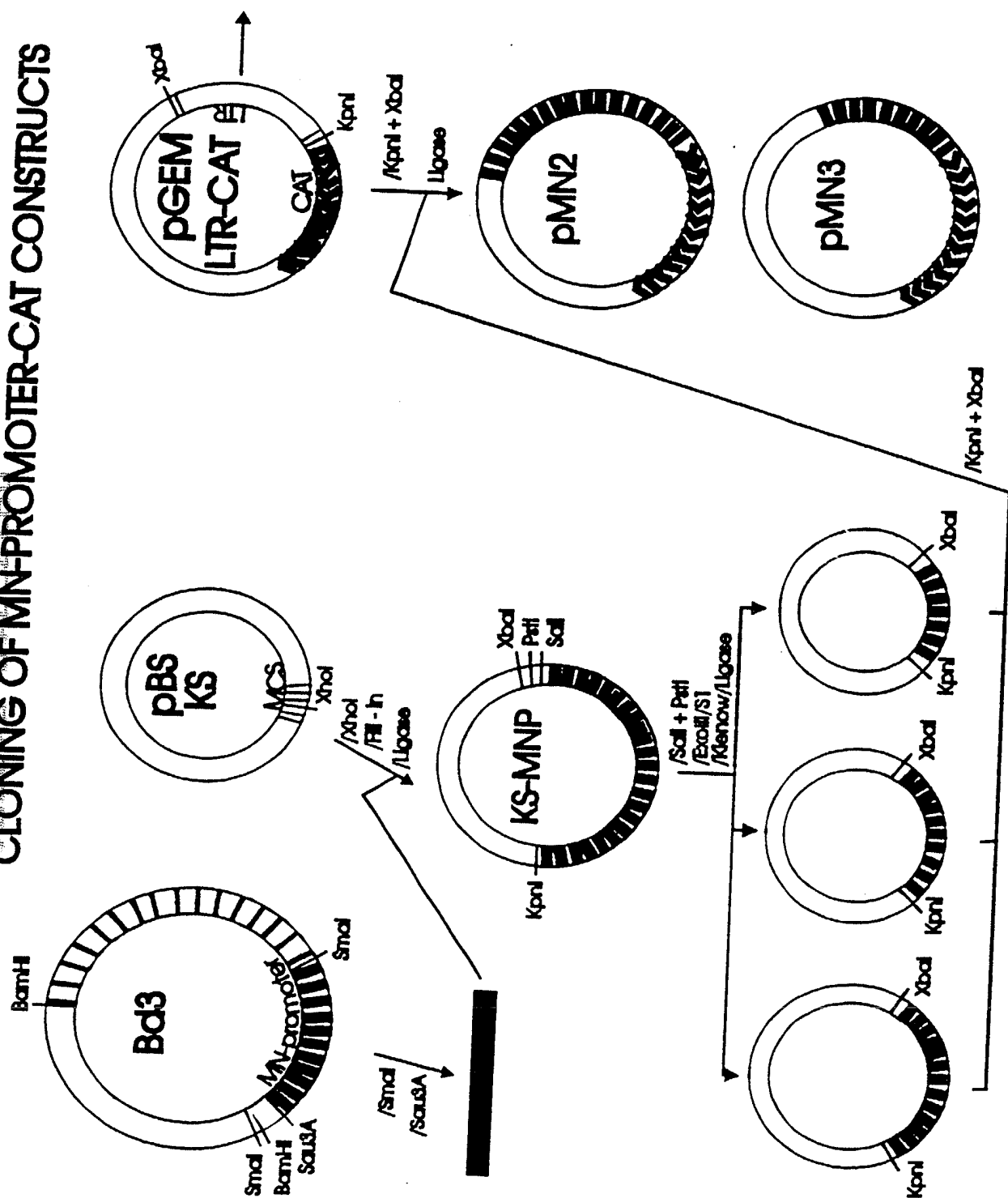


FIG. 28

STRUCTURE OF MN PROMOTER - CAT CONSTRUCTS

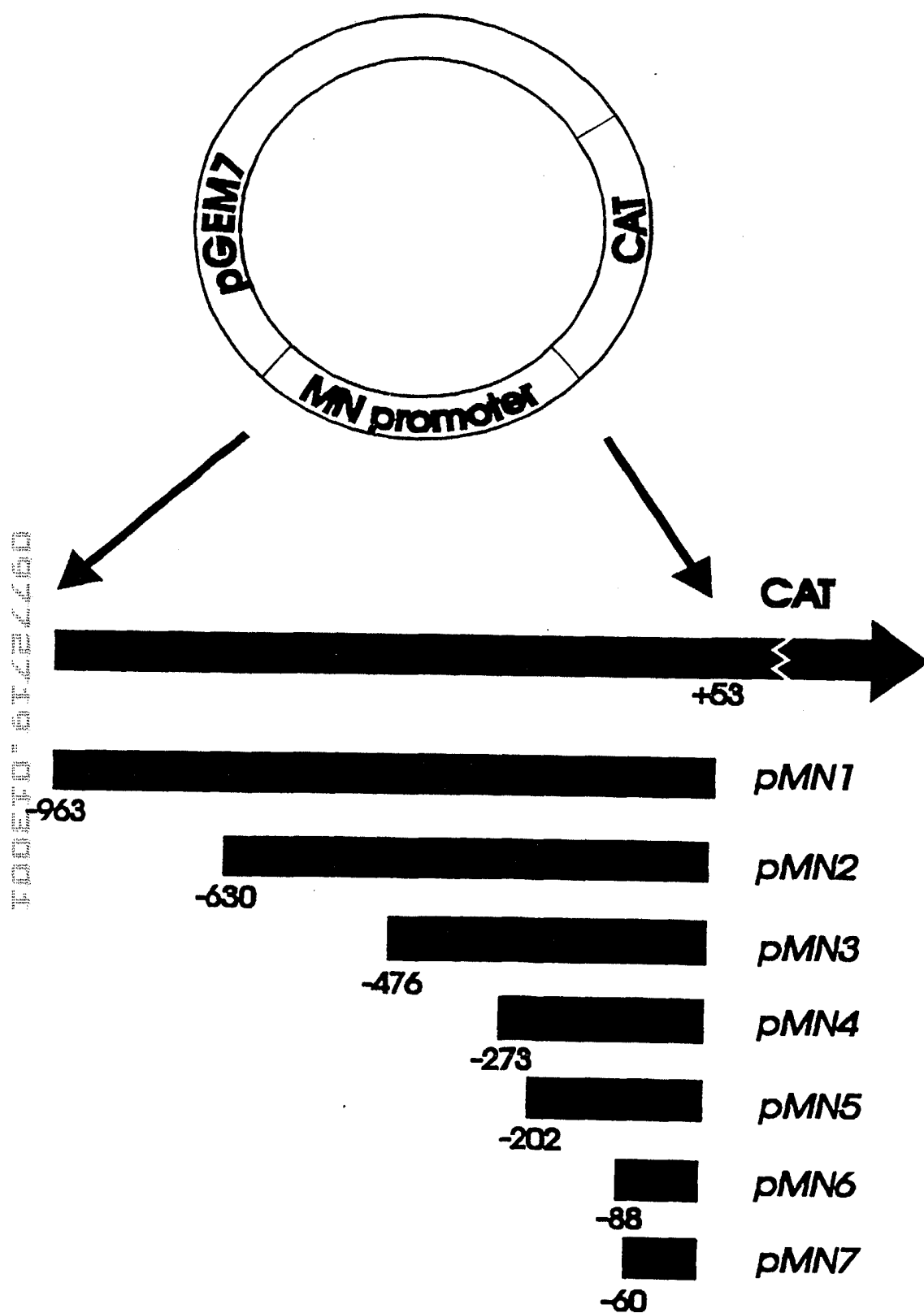


FIG. 29